

METHODS FOR IDENTIFYING SUITABLE NUCLEIC ACID PROBE SEQUENCES FOR USE IN NUCLEIC ACID ARRAYS

ABSTRACT OF THE DISCLOSURE

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Methods of identifying a sequence of a probe, e.g., a biopolymeric probe, such as a nucleic acid, for use as a surface immobilized probe for a target molecule of interest, e.g., a target nucleic acid, are provided. A feature of the subject methods is that a set of candidate sequences is evaluated for full-length synthesis probability, e.g., by evaluating the candidate sequences' depurination susceptibility. The subject invention also includes algorithms for performing the subject methods recorded on a computer readable medium, as well as computational analysis systems that include the same. Also provided are nucleic acid arrays produced with probes having sequences identified by the subject methods, as well as methods for using the same.

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